REMARKS

Reconsideration of the application as amended is respectfully requested. The specification has been amended to correct typographical errors. No new matter has been added by virtue of the amendments to the specification.

Claims 3, 4, 15, 16 and 17 have been amended to recite that the polynucleotide of the embodiments claimed therein encodes a full-length polypeptide having PP2A-4 activity. Support for this amendment is found throughout the application, and specifically at paragraph 0042, paragraph 0053, and in Example 6. Claims 3, 4, 15, 16, and 17 have also been amended to clarify the Markush language and to more particularly point out and distinctly claim the invention as embodied therein. Claims 5, 6, and 7 have been amended to correct the antecedent basis. Claims 8 through 10, 13, and 14 have been cancelled. Claim 15 has been amended to recite that the seed comprises a transgene. Support for the recitation of "transgene" is found throughout the application, and specifically in Examples 8 and 9. Claim 16 has been amended to independent form and to recite that the expression vector also comprises a regulatory sequence. Support for this amendment appears throughout the application, and specifically at paragraph 0076 and at paragraph 0087. Claims 19 and 20 have been amended to depend from claim 17, which has been placed in independent form as suggested by the Examiner. New claims 21, 23, 25, and 27, which depend from claim 1 and are directed to transgenic plant cells of various plant species, have been added. New claims 22, 24, 26, and 28, which depend from claim 2 and are directed to transgenic plant cells from various species, have been added. New claims 29-33 are picture claims directed to the various Markush group members recited in claim 15. New claim 34 is a picture claim directed to a Markush group member recited in claim 17. Support for new claims 21-34 is found throughout the application and in the claims as filed. New claim 35 is directed to an expression vector within the scope of the present invention. Support for new claim 35 is found throughout the application, and specifically at paragraphs 0052-0053, at paragraphs 0057-0058, at paragraph 0076, and at paragraph 0087. A clean copy of the claims is attached hereto as Appendix A, for the convenience of the Examiner. No new matter has been added by virtue of the amendments to the claims.

Rejections under 35 U.S.C. § 112

Claims 3-10, 13-16, and 19-20 stand rejected under § 112, first paragraph, as failing to meet the written description requirement for the genus of nucleic acids that hybridize to SEQ ID NO:8 or its complement or for the genus of nucleic acids having at least 90% sequence identity with SEQ ID NO:13. The Examiner takes the position that a representative number of species falling within the claimed genus have not been described. This rejection is respectfully traversed.

The Examiner admits that no less than five different type 2A phosphatase polypeptides demonstrating 89-91% sequence identity and 93-94% sequence similarity to SEQ ID NO:13 are disclosed in the application. The facts of *University of California v. Eli Lilly and Co.*, 43 USPQ2d 1398 (Fed. Cir. 1997) are thus inapposite to the instant application, since the patent at issue in *Lilly* disclosed only a single cDNA species encoding rat insulin to support a claim to the genus of all cDNAs encoding mammalian insulin.

The Federal Circuit has clearly stated that the written description requirement must be applied in the context of the particular invention and the state of the knowledge in the relevant art. *Capon v. Eshhar,* 76 USPQ2d 1078, 1084 (Fed.Cir. 2005). The determination of what is needed to support generic claims to biological subject matter depends on such factors as the existing knowledge in the particular field, the extent and content of the prior art, the maturity of the science or technology, and the predictability of the aspect at issue. *Id.* at 1085. The Federal Circuit has recognized that the state of the art in biotechnology has progressed, acknowledging, for example, that the complete amino acid sequence of a protein may put one in possession of the genus of DNA sequences encoding it, *In re Wallach*, 71 USPQ2d 1939, 1942 (Fed. Cir. 2004). The Federal Circuit has further taken judicial notice of the statement in the written description guidelines set forth in the MPEP that the written description requirement can be met by showing:

> . . . that an invention is complete by disclosure of sufficiently detailed, relevant identifying characteristics. . .*i.e.*, complete or partial structure, other physical and/or chemical properties, *functional characteristics when coupled with a known or disclosed correlation between function and structure*, or some combination of such characteristics.

Enzo Biochem Inc. v Gen-Probe Inc., 63 USPQ2d 1609, 1613 (Fed. Cir. 2002) (*1 emphasis in original*).

Submitted herewith as Appendix B is a copy of Lizotte, *et al.* (1999) Gene **234**, 35-44, which discloses at page 37, col. 1, that the amino acid sequences of PP2A serine/threonine phosphatase catalytic subunits ". . . are highly conserved in eukaryotes as distantly related as *Arabidopsis thaliana*, humans, and yeast." Lizotte *et al.* further discloses that the *A. thaliana* PP2A gene is capable of complementing a conditional lethal yeast PP2A mutant, indicating that the function of PP2A is also conserved among eukaryotes.

The correlation between structure and function of the PP2A serine/threonine phosphatase catalytic subunit was known at the priority date of the instant application. As a matter of law, therefore, the disclosure of five known PP2A species in the instant application adequately describes the genus of full-length polypeptides having PP2A-4 activity which can be transformed into plants to increase stress tolerance in accordance with the present claims. Accordingly, withdrawal of the written description rejection of claims 3-10, 13-16 and 19-20 is respectfully requested.

Claims 3-10, 13-16, and 19-20 stand rejected under § 112, first paragraph, as not being enabled for the entire scope of the claims. The Examiner takes the position that the function of nucleic acid sequences that hybridize to SEQ ID NO:8 or that encode polypeptides having at least 90% sequence identity to SEQ ID NO:13 is unpredictable. The Examiner cites Whisstock et al. to support the premise that structurally homologous sequences are not always functionally homologous. This rejection is respectfully traversed.

At page 324, third full paragraph, Whisstock et al. state that:

> [h]aving identified putative homologues, multiple sequence alignments enable identification of conserved residues, the literature may provide crucial information about the family as a whole and the role of conserved residues, and phylogenetic trees can provide information as to whether an unknown protein clusters with a particular functional grouping. In general, if an unknown protein shares significant sequence similarity with a family of known function, possesses the 'right essential conserved residues' (e.g. active-site residues) then a prediction as to function (proteinase, exonuclease, etc) can reasonably be proposed. In addition, if the unknown also forms part of a well-supported functional cluster or clade within a phylogenetic tree then a more detailed level of functional prediction may be possible. *(citations omitted)*

Submitted herewith is the Declaration Pursuant to 37 C.F.R. § 1.132 of Ruoying Chen, which presents alignments of SEQ ID NO:13 with the sequences of the five known PP2A homologs disclosed in Table 4 of the application. The Declaration clearly shows that there is significant sequence similarity with the serine/threonine phosphatase family, including conservation of the serine/threonine phosphatase motif.

Thus contrary to the Examiner's position, the present application provides ample guidance to allow those of ordinary skill to make and to use the entire genus of serine/threonine phosphatase sequences in accordance with the presently claimed invention. In fact, the yeast complementation assay of Lizotte et al. provides an effective functional assay to identify additional serine/threonine phosphatases suitable for transformation into plants to enhance stress tolerance. Withdrawal of the rejection of claims 3-10, 13-16, and 19-20 under § 112, first paragraph for lack of enablement is therefore respectfully requested.

Rejection under 35 U.S.C. § 102

Claims 13-14 and 16 stand rejected under § 102(b) as being anticipated by Arino et al.

Cancellation of claims 13 and 14, and the amendment to claim 16, are believed to obviate this rejection as applied to those claims.

Insofar as the rejection may be applicable to new claim 35, neither the alignment of Arino et al. as cited by the Examiner, nor the underlying reference (Plant Mol. Biol. (1993) **21**, 475-485, submitted in the Supplemental Information Disclosure filed herewith) discloses the expression vector of claim 35. Withdrawal of the rejection under § 102(b) over Arino et al. is therefore respectfully requested.

In light of the amendments, the arguments and the evidence presented, Applicants submit that all of the rejections contained in the Office Action dated February 15, 2006 have been overcome, and that the application is in condition for allowance or appeal. Should the Examiner wish to discuss the application further, she is invited to telephone the undersigned. If any additional fees are due with respect to this submission, authorization is hereby given to charge such fees, or to credit any overpayment, to Deposit Account No. 02-1197.

Respectfully submitted,

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